

Abstract of the Disclosure

The invention concerns methods for applying evolutionary analyses to a set of aligned homologous protein sequences for the purpose of predicting a consensus model for the folded secondary structure of a protein family, identifying distant homologs and denying distant homology, assigning functional behavior to protein families, identifying protein pairs that interact as they function, identifying episodes of sequence evolution where functional behavior within a family is changing, and identifying specific chemical units of the protein that change in concert with changes in functional behavior. Accordingly, this invention is relevant to the use of genomic information to understand homology, fold, behavior and function in proteins.